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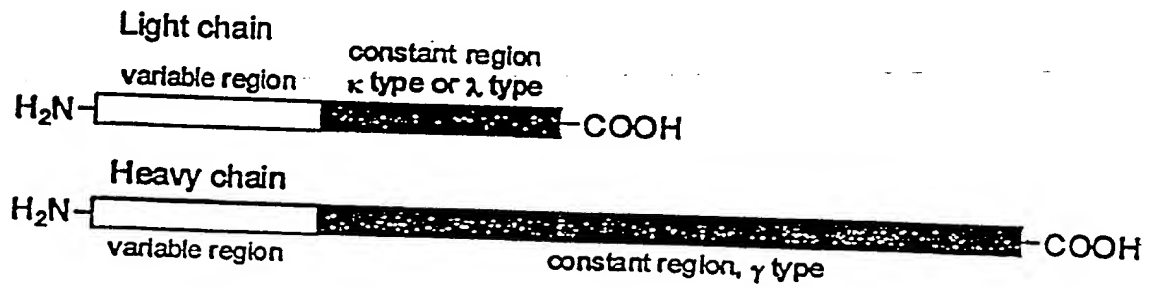


FIG. 1

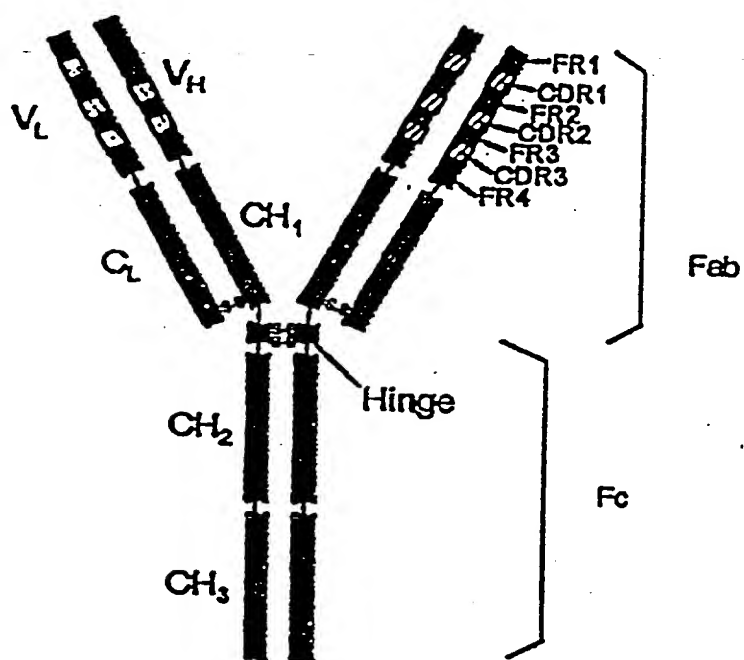


FIG. 2

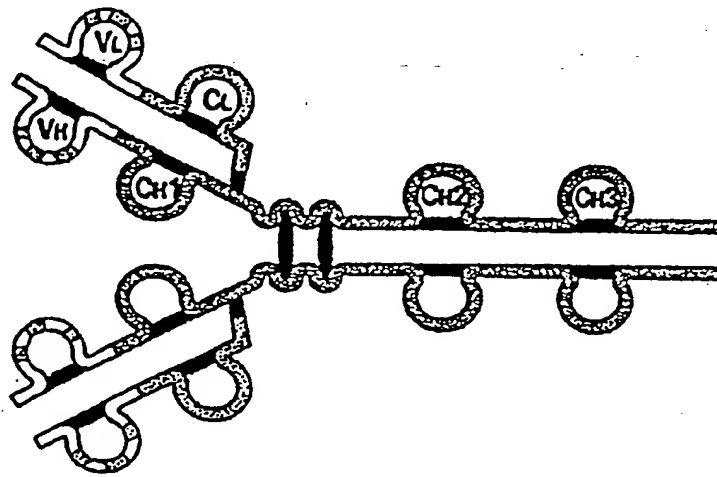
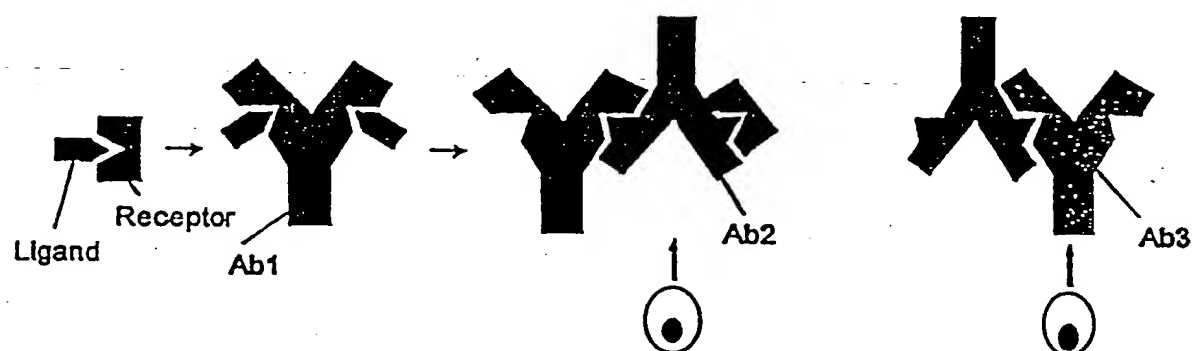


FIG. 3

**FIG. 4**

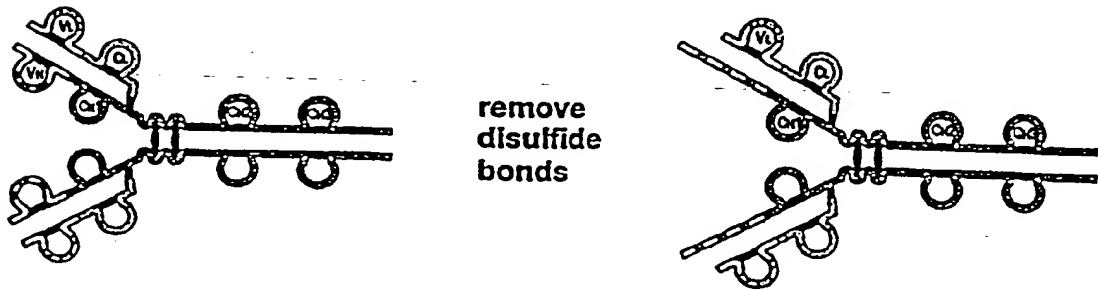


FIG. 5

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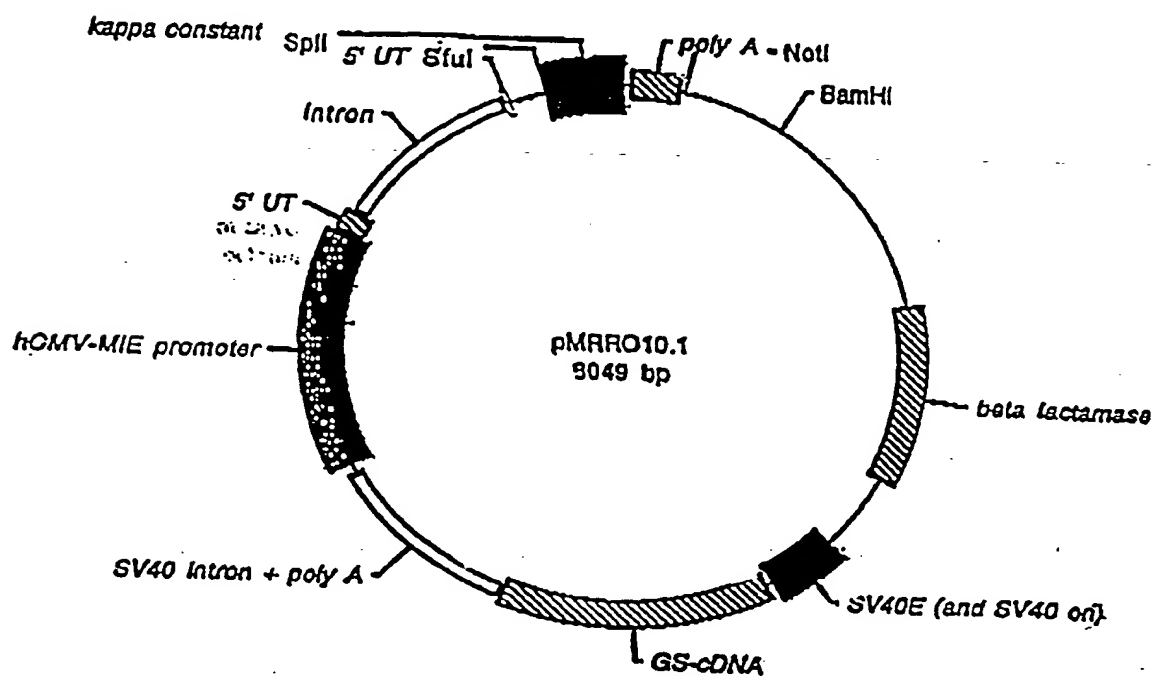


FIG. 6A

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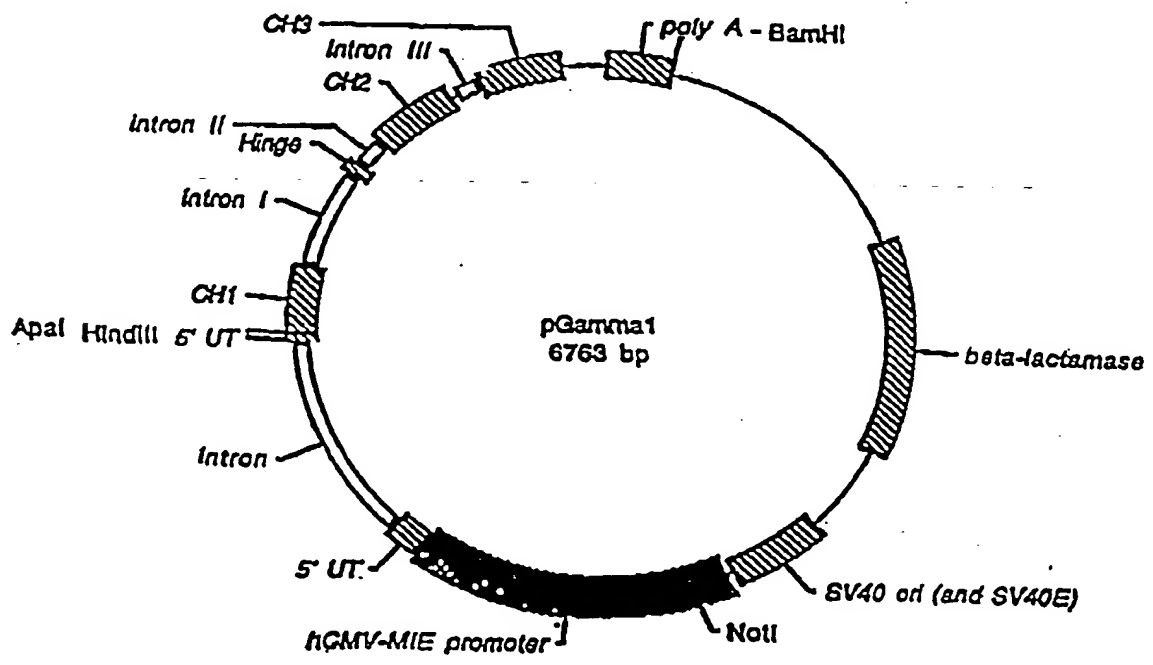


FIG. 6B

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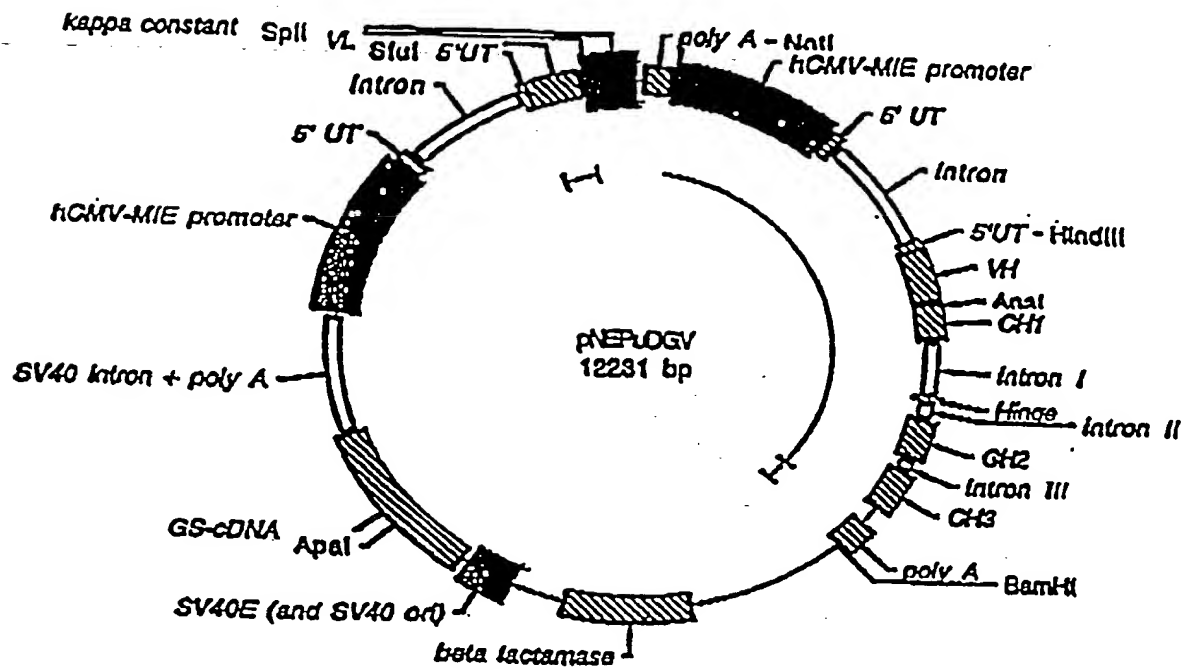


FIG. 6C



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ConVL1

EcoRI  
GAA TTC

6

-19 (Leader)

Met Ala trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser Ala Gln Ala  
ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GCT GCC CAA AGT GCC CAA GCA  
63

VL:

1 10 20  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr  
GAT ATC CAA ATG ACA CAA AGT CCT AGT AGT TTG AGT GCT AGT GTG GGA GAT CGG GTG  
ACA 123

21 30 40  
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys  
Pro  
ATC ACA TGT CGG GCT AGT CAA AGT ATC AGT AAC TGT TTG GCT TGG TAT CAA CAA AAG  
CCT 183

41 50 60  
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro  
Ser  
GGA AAG GCT CCT AAG TTG TTG ATC TAT GCT GCT AGT AGT TTG GAG AGT GGA GTG CCT  
AGT 243

61 70 80  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Arg Phe Thr Leu Thr Ile Ser Ser Lys Gln  
Pro  
CGG TTC AGT GGA AGT GGA AGT GGA ACA CGG TTC ACC TTG ACC ATC AGT AGT TTG CAA  
CCT 303

81 90 100  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Leu Pro Trp Thr Phe Gly  
Gln  
GAG CAT TTC GCT ACC TAT TAT TGT CAA CAA TAT AAC AGT TTG CCT TGG ACC TTC GGA  
CAA 363

101  
Gly Thr Lys Val Glu Ile Lys  
GGA ACC AAG GTG GAG ATC AAG GAA TTC  
EcoRI

390

FIG. 7A

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ConVH1

EcoRI  
GAA TTC

6

-19 (Leader)

Met Ala trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala  
 Gln Ser Ala Gln Ala  
 ATG GCT TGG GTG TGG ACC TTG CTA TTC CTG ATG GCA GOT GCC  
 CAA AGT GCC CAA GCA 63

VL:

1 10 20  
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
 Gly Ala Ser Val Lys Val  
 CAG GTT CAG CTG GTG CAG TCT GGC GCT GAG GTG AAG AAG CCT  
 GGC GCT TCT GTG AAG GTG 123

21.  
40

30

35A 35B

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Ala Ile  
 Ser Trp Asn Trp Val Arg Gln Ala  
 TCT TGC AAG GCT TCT GGC TAC ACA TTC ACA TCT TAC GCT ATA  
 TCT TGG AAT TGG GTG AGG CAG GCT 189

41

50

60

Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Gly Asn  
 Gly Asp Thr Asn Tyr Ala  
 CCT GGC CAG GCC CTG CAG TGG ATG GGC TGG ATA AAT GGA AAT  
 GGA GAT ACA AAT TAC GCC 249

61

70

80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser  
 Thr Ser Thr Ala Tyr Met  
 CAG AAG TTC CAG GGA AGG GTG ACT ATA ACT GCT GAT ACT TCT  
 ACT TCT ACT GCT TAC ATG 309

81

82A 82B 82C

90

100  
 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr  
 Cys Ala Arg Ala Pro Gly Tyr Gly Ser  
 CAG CTG TCT TCT CTG AGG TCT CAG GAT ACT GCT GTT TAC TAC  
 TGC GCT AGG GCT CCT GGC TAC GGC TCT 378

101

110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 GAT TAT TGG GGA CAG GGA ACA CTG GTT ACA GTT TCT TCT GAA TTC  
 423

FIG. 7B

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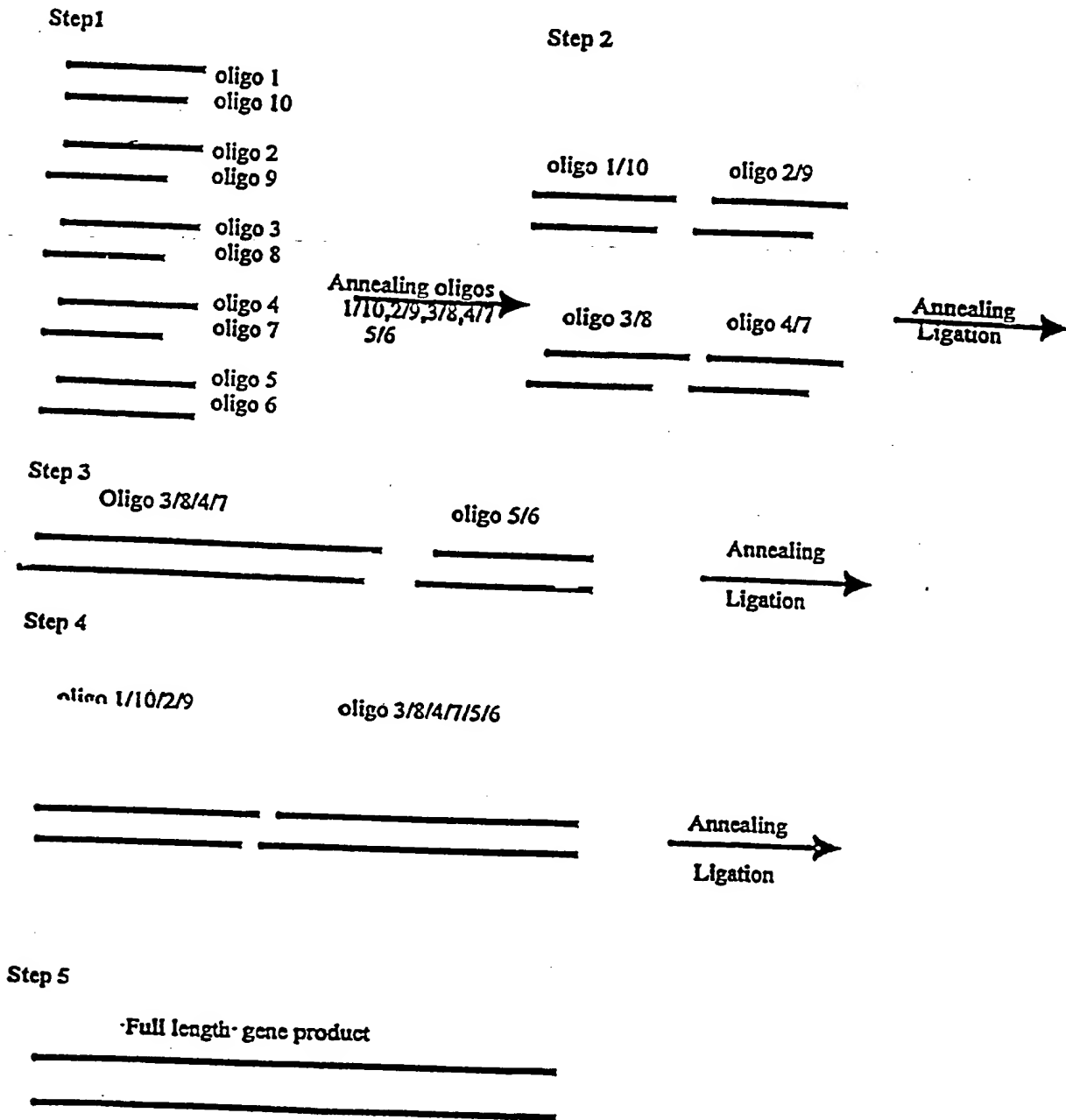


FIG. 8

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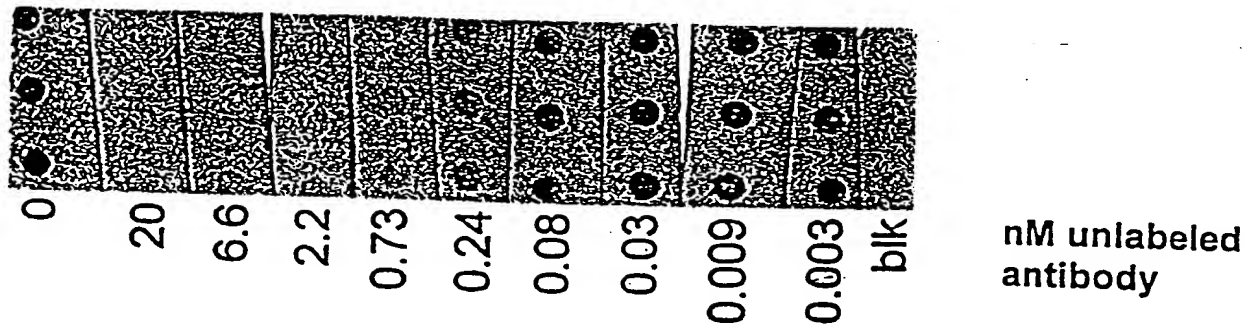
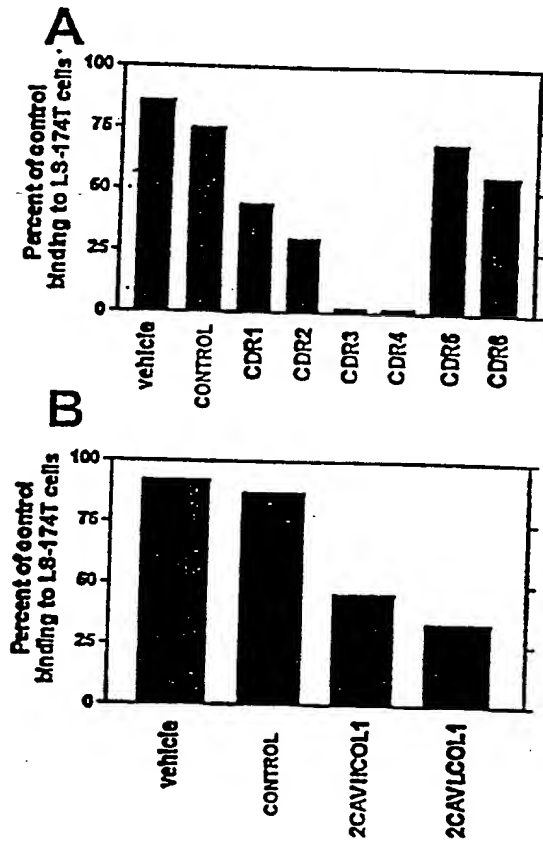


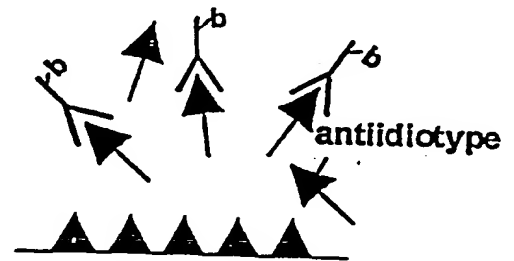
FIG. 9



**C**



**D**



FIGS. 10A-D

cstacy  
 DSABL-1 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTGTCAGTTGGAGAGAAGGTTACTATG 0.05  
 PAGE 83  
 DSABL-1c  
 GCAGCTCATAGTAACCTTCTCTCCAACTGACACAGCTAGGGAGGATGGAGACTGTGACATCACAATGTCTGC  
 TTGGGC 0.05 PAGE 78  
 MSAL-CDR1-1 ~~1~~ GCT in MSAL-VAC-CDR1-1  
 AGGTGGCTCGGCAGCCTCCGAAGCAGCCCGCTCCAGAGCCCGCTGCTCCGATGGTACCAGCAGAAACCAG  
 GGCAGTCTCCTAAA 0.05 PAGE 84  
 MSAL-CDR1-1c  
 CTGCCCTGGTTTCTGCTGGTACCATCGGAGCAGCGGGCTCTGGAGCGGGCTGCTTCGGAGGCTGCCGAC  
 0.05 PAGE 89

HMV1 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTGTCAGTTGGAGAGAAGGTTACTATGAGGCTAAGTCCAGT  
 HMV2 CAGAGCCTTTTATATAGTACATCAAAAGATCTACTTGGCCTGGTACCGACAGAACCAAGGCACTCTCCTAAA  
 HMV3 CTGCTGATTTACTGGGCTOACTAGGCAATCTGGGCTCCTGATCGCTTCAGAGGCGGTGATCTGCG  
 HMV4 CCACAGCATAITATAGATATCCTCCGACGTTCCGCTGAGGACCAAGCTGGAAATCAAGGGAATTC  
 HMV5 AGGCGCTGTGAAGGATCAGGGAAGGCAAGTCCCTAGTGGATGCCAGTAATCAGCAATTTAGGACA  
 HMV6 CTGCCCTGGTTCTGCTGTAACAGGCCAAGTACATCTTTGATTGCTACTATATAAGGCTCTGACTGGCTT  
 HMV10 AGGCGCTATATAGCTTCTCTCCACTCAGACAGCTAGGGAAGATGAGAGCTGTGACATCAGATGCTCTGCGG  
 HMV6 GATTCGCGTTTCATTTCCAGTTGGTCCCTCCAGCGAGCTCCGAGATATCTATAATATGCTGTGCGTAATTAAC

#### HMVL4

ARG AGA TTT CAG TCT CAG CAT CAG CAG TGT GAA GGG TGA AGA COT GGG  
 AGT TTA TTA C

#### HMVL7

TG CAA GGT GTT CAG COT TCA CAG TGA TGG TGA GAG TGA AAT OTG  
 TCC CAG ATC C

FIG. 11

- A** MSA-63 epitope DNA  
 GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA CCG CTC GTC  
 CAG AGC AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC GGC GAC GGC AGC  
 TGC AGC CGA CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG CTG CTG  
 CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC
- B** MSA-63 protein sequence (Start residue 143 end residue 233)  
 Gln Pro Ser Glu Ala Ser Ser Gly Glu Val Ser Gly Asp Glu Ala Gly Glu Gln Val Ser Ser Glu Thr Asn Asp  
 Lys Glu Asn Asp Ala Met Ser Thr Pro Leu Pro Ser Thr Ser Ala Ala Ile Thr Leu Asn Cys His Thr Cys Ala  
 Tyr Met Asn Asp Asp Ala Lys Cys Leu Arg Gly Glu Gly Val Cys Thr Thr Gln Asn Ser
- C** MSA-63 oligo
- MSA1  
 GTC GGC AGC CTC CGA AGC AGC CCG CTC CAG AGC CCG CTG CTC CGA
- MSA2  
 AGC CCG CTG CTC CGA CCG CTC GTC CAG AGC AGC CTC TGC TTG CTG
- MSA3  
 AGC CTC TGC TTG CTG TTC CTC TTG CTG CGA TAC AGC TGC GGC GAC
- MSA4  
 TAC AGC TGC GGC GAC GGC AGC TGC AGC CGA CGA TAC TGC GAC TTG
- MSA5  
 CGA TAC TGC GAC TTG ACG GTG TGC ACG CGA ATG TAC TTG CTG CTG
- MSA6  
 ATG TAC TTG CTG CTG CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG
- MSA7  
 CGA TTC ACG GAC GCG CCG CTC CCG CAG ACG TGC TGC GTC TTG AGC

FIGS. 12A-C

- A** SP-10 Epitope  
 GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT GAG CAG  
 GCC TCG GGT GAA CAG CCT TCA GGT GAG CAC GCT TCA GGG GAA CAG GCT TCA GGT  
 JCA CCA ATT TCA AGC ACA TCT ACA GGC ACA ATA TTA AAT TGC TAC ACA TGT GCT TAT  
 ATG AAT GAT CAA GGA AAA TGT CTT CGT GGA GAG GGA ACC TGC ATC ACT CAG AAT TC
- B** SP-10 protein sequence  
 Gln Pro Ser Gly Glu His Gly Glu Gln Pro Ser Gly Glu Gln Ala Ser Gly Glu Gln Pro Ser gly Glu His Ala  
 Ser Gly Glu Gln Ala Ser Gly Ala Gln Ile Ser Ser Thr Ser Thr Gly Thr Ile Leu Asn Cys Tyr Thr Cys Ala  
 Tyr Met Asn Asp Gln Gly Lys Cys Leu Arg Gly Glu Gly Thr Cys Ile Thr Gln Asn
- C** Oligo SP1:  
 GAA TTC CAG CCT TCA GGT GAA CAT GGC TCC GGT GAA CAG CCT TCT GGT GAG CAG  
 GCC TCG GGT GAA CAG CCT TAG
- Oligo SP2:  
 GTG AGC ACG CTT CAG GGG AAC AGG CTT CAG GTG CAC CAA TTT CAA GCA CAT CTA  
 CAG GCA CAA TAT TAA ATT GCT
- Oligo SP3:  
 ACA CAT GTG CTT ATA TGA ATG ATC AAG GAA AAT GTC TTC GTG GAG AGG GAA CCT  
 GCA TCA CTC AGA ATT C
- Oligo SP3a(3Cys->Ala):  
 ACA CAG CAG CTT ATA TGA ATG ATC AAG GAA AAG CAC TTC GTG GAG AGG GAA  
 CCG CAA TCA CTC AGA ATT C
- Oligo SP4:  
 GAA TTC TGA GTG ATG CAG GTT CCC TCT CCA CGA AGA CAT TTT CCT TGA TCA TTC ATA  
 TAA GCA CAT GTG TAG CAA TTT A
- Oligo SP4a (3Cys->Ala):  
 GAA TTC TGA GTG ATT GCG GTT CCC TCT CCA CGA AGT GCT TTT CCT TGA TCA TTC ATA  
 TAA GCT GCT GTG TAG CAA TTT A
- Oligo SP5:  
 ATA TTG TGC CTG TAG ATG TGC TTG AAA TTG GTG CAC CTG AAG CCT GTT CCC CTG AAG  
 CGT GCT CAC CTG AAG GCT
- Oligo SP6:  
 GTT CTC CCG AGG CCT GCT CAC CAG AAG GCT GTT CAC CGG AGC CAT GTT CAC CTG  
 AAG GCT GGA ATT C

FIGS. 13A-C



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**LDH-C<sub>4</sub> Epitope:**

**Oligo LDH1:**

TCG TGC CAG TTC CTC GTC GAC TAG CTC TTC GAC TAG CTC CTG CTG CTC TTG TCG GTC  
ACG GAA TTC

**Oligo LDH2:**

GAA TTC CGT GAC CGA CAA GAG CAG CAG GAG CTA GTC GAA GAG CTA GTC GAC GAG  
GAA CTG GCA CGA CGG GTT CGT

**FIG. 14**

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Leader:

-19

Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Gln Ser Ala Gln Ala  
ATG GCT TGG GTG TGG ACC TTA CTC CTA TTC CTG ATG GCA GCT GCC CAA AGT GCC CAA GCA

Ala  
V<sub>1</sub>  
GCT in vaccine

10  
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gln Gln Lys Val Thr  
CAC ATT GTG ATG TCA CAG TCT CCA TCC TCC CTA GCT GTG TCA GTT GGA CAG AAG GTT ACT

21 Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Tyr Ser Ser Leu Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys Pro  
ATG AGC TGC AAG TCC AGT CAG AGC CTT TTA TAT TAT AGT AGC AAT CAA AAG ATC TAC TTG GCC TGG TAC CAG CAG AAA CCA  
27 A B C D E F  
30  
40

41 Gln Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gln Val Pro Asp  
GGG CAG TCT CCT CCT AAA CTG CTG ATT TAC TGG GCA TCC ACT AGG GAA TCT GGG GTC CCT GAT  
50  
60

61 Arg Phe Thr Gln Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala  
CGC TTC ACA GGC GGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT GTG AAG GCT  
70  
80

81 Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gln Gly  
GAA GAC CTG GCA GTT TAT TAT TAC TGT CAG CAA TAT TAT AGA TAT CCT CCG ACG TTC GGT GGA  
90  
100

101 Gly Thr Lys Leu Gln Ile Lys Arg  
GGC ACC AAG CTG GAA ATC AAA CCG

FIG. 15

## 2CAVHCOL1

- VHC1 5'GAATTCATGGCTTGGGTGTGGACCTTGCTATTCTGATGGCAGCTGOCCAAAGTGCCC  
AAGCACAGATOCAGTTGGTGCA 3'
- VHC2 5'GTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTOOGCTAAGGCTTC  
TGGGTATACCTTCACAAACTAG 3'
- VHC3 5'GAATGAACTGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGAT  
AAACACCTACACTGGAGAGOCOAACA 3'
- VHC4 5'TATGCTGATGACTTCAAGGGACGGTTTGCTTCTCTTTGGAAACCTCTGCCAGCACT  
GCTATTTGCAGATCAACACCT 3'
- VHC5 5'CAAAAATGAGGACAAGGCTACATATTTGCTGCAAGAGCCTACTATGGTAAATAC  
TTTGACTACGAATTC 3'
- VHC6 5'GAATTOGTAGTCAAAGTATTTACCATAGTAGGCTCTTGCAGCAAATATG 3'
- VHC7 5'TAGCCGTGTCTCATTTTTGAGGTTGTTGATCTGCAAATAGGCAGTGCTGGCAGA  
GGTTTCCAAAGAGAAGGCAAACCGT 3'
- VHC8 5'CCCTTGAAGTCATCAGCATATGTTGGCTCTOCAGTGTAGGTGTTTATCCAGCCCAT  
CCACTTTAAACCTTTCTCTGGAGC 3'
- VHC9 5'CTGCTTCAOCCAGTTCATTCCATAGTTTGTGAAGGTATACCCAGAAGCCTTAGGG  
AGATCTTGACTGTCTCTCCAGGCT 3'
- VHC10 5'TCTTCAGCTCAGGTCCAGACTGCACCAACTGGATCTGTGCTTGGGCACTTTG GGC  
AGCTGOCATCAGGAATAGCAAGGTCCACACCCAAGCCATGAATTC 3'

FIG. 16A

**2CAVLCOL1**

- VLC1 5'AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTT  
AOCATA 3'
- VLC2 5'ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAAACC  
AGGGCAG 3'
- VLC3 5'TCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCT  
TCACTGGCAGT 3'
- VLC4 5'GGATATGGGACGGATTTCACCTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCA  
GTTTAT 3'
- VLC5 5'TTCTGYCAGCAGGATTATAGCTCTCCGCTCACGTTCCGGTGCTGGGAACCAAGCTGGAG  
CTGAAAGAATTC 3'
- VLC6 5'GAATTCTTTCAGCTCCAGCTTGGTCCCAGCACCGAACGTGAGCGGAGAGCTATAATC  
CTGCTGACAGAAATAAACTGC 3'
- VLC7 5'CAGGTCTTCAGCCTGCACAGTGCTGATGGTGAAAGTGAAATCCGTCCCATATCCA  
CTGCCAGT 3'
- VLC8 5'GAAGCGATCAGGGACTCCAGTGTAGCGATTGGATGCATAGTATATCAGCAGTTTAG  
GAGACTGCCCTGG 3'
- VLC9 5'TTCTGTGTTGGTACCAAGCTACATCATTACTCACACTCTGACTGGCCTTGCAGGTTA  
TGGTAAC 3'
- VLC10 5'CCGTCTCCTGCTGATACAAGCAGGAATTTGGGAGTCTGGGTCATCACAATACTT  
GCTTGGGC 3'
- VLC11 5'TTCGCTCAGCAGGATTATAGCTCTCCGCTCACGTTCCGGTGCTGGGAACCAAGCTGG  
AGCTGAAAGAATC 3'
- VLC12 5'GAATTCTTTCAGCTCCAGCTTGGTCCCAGCACCGAACGTGAGCGGAGAGCTATAA  
TCCTGCTGAGCGAAATAAACTGC 3'

**FIG. 16 B**